SEQUENCE LISTING

<110> Sim, Gek-Kee Yang, Shumin Sellins, Karen S. <120> NOVEL FORMS OF T CELL COSTIMULATORY PROTEINS, NUCLEIC ACID MOLECULES, AND USES THEREOF <130> IM-1-C1-PCT <140> not yet assigned <141> 1999-03-19 15 媚 <150> 60/078,765 ff <151> 1998-03-19 <150> 09/062,597 <151> 1998-04-17 T <160> 65 1.1 Ŧij. <170> PatentIn Ver. 2.0 ß į, sie <210> 1 <211> 2830 <212> DNA <213> Canis familiaris <220> <221> CDS <222> (337)..(1248) <400> 1 gtgctttgtc ctagccacac tctctgaggt ggctgacaaa aagggacagc agaaccagct 60 tecteaagtt atacataaca tetacacate ecetgetttg aettaaatae tgetggtaat 120 gaacatcagc tagatcttcc agcgagtaaa aggaagttgg aaaggggatt gcctctggta 180 tatcacccaa agaaaagctg agcaacttgc cattattttg gagacagcaa gaaaggaaca 240 teteagaact ggggeeteat cetttgaegt tittgttittgt tittgttetaa cacaagaaaa 300 aaaaaaaaga ggagttatcc ttcagcagca gaagcc atg gat tac aca gcg aag 354 Met Asp Tyr Thr Ala Lys

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acccctgatg gagaccacat cctctggatt gcggctctgc ttgtaatgtt ggtcattttg 780
tgtgggatgg tgttctttct aacactaagg aaaaggaaga agaagcagcc tggcccctct 840
catgaatgtg aaaccaacaa agtggagaga aaagaaagtg agcagaccaa ggaaagagta 900
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tcagcagcag cagaagcc atg gat tac aca gcg aag tgg aga aca cca cca Met Asp Tyr Thr Ala Lys Trp Arg Thr Pro Pro 1 5 10	111
ctc aaa cac cca tat ctc aag gtc tct cag ctc ttg gtg cta gct agt Leu Lys His Pro Tyr Leu Lys Val Ser Gln Leu Leu Val Leu Ala Ser 15 20 25	159
ctc ttt tac ttc tgt tca ggc atc atc cag gtg aac aag aca gtg aaa Leu Phe Tyr Phe Cys Ser Gly Ile Ile Gln Val Asn Lys Thr Val Lys 30 35 40	207
gaa gta gca gta ctg tcc tgt gat tac aac att tcc act aca gaa ctg Glu Val Ala Val Leu Ser Cys Asp Tyr Asn Ile Ser Thr Thr Glu Leu 45 50 55	255
atg aaa gtt cga atc tat tgg caa aag gat gat gaa gtg gtg ctg gct Met Lys Val Arg Ile Tyr Trp Gln Lys Asp Asp Glu Val Val Leu Ala 60 65 70 75	303
gtc aca tct gga caa acg aaa gtg tgg tcc aag tat gag aat cgc acc Val Thr Ser Gly Gln Thr Lys Val Trp Ser Lys Tyr Glu Asn Arg Thr 80 85 90	351
ttt gct gac ttc acc aat aac ctc tcc atc gtg att atg gct ctg cgc Phe Ala Asp Phe Thr Asn Asn Leu Ser Ile Val Ile Met Ala Leu Arg 95 100 105	399
ctg tca gac aat ggc aaa tac acc tgt atc gtt caa aag act gaa aaa Leu Ser Asp Asn Gly Lys Tyr Thr Cys Ile Val Gln Lys Thr Glu Lys 110 115 120	

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							_		_	-	atg Met 135		-	-	-	495
-	_			-		_			-		Gly				cat His 155	543
-					-	-					ggt Gly			_		591
				-							aat Asn		-			639
				-	_	-		-	_		act Thr		_	_	-	687
_	-					-			_		gtg Val 215	-		-	_	735
		-			_		_				tgg Trp			_	-	783
taad	catte	gtt d	ctgaç	ggagt	t to	tact	gtgt	aaa	atct	aaa	aaga	aaat	aa c	ctcag	ccaga	843
taca	attti	egg a	aatta	atgta	at gt	taac	ettte	g ata	gcat	ttc	ttgt	attt	tt a	gacc	cataa	903
atga	ataa	tga a	agtga	atatt	ig to	gactt	gtta	a ago	gtcac	tgt	acag	gtat	gg c	cata	atgtt	963
act	aatti	tta 1	tttc	cttta	aa ta	aaaco	cttct	aaa	acto	gaga	cato	caaa	aa a	ıaaaa	aaaaa	1023
a													•			1024

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<211> 235

<212> PRT

<213> Canis familiaris

<400> 12

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Leu Lys Val Ser Gln Leu Leu Val Leu Ala Ser Leu Phe Tyr Phe Cys 20 25 30

Ser Gly Ile Ile Gln Val Asn Lys Thr Val Lys Glu Val Ala Val Leu 35 40 45

Ser Cys Asp Tyr Asn Ile Ser Thr Thr Glu Leu Met Lys Val Arg Ile 50 55 60

Tyr Trp Gln Lys Asp Asp Glu Val Val Leu Ala Val Thr Ser Gly Gln 65 70 75 80

Thr Lys Val Trp Ser Lys Tyr Glu Asn Arg Thr Phe Ala Asp Phe Thr . 85 90 95

Asn Asn Leu Ser Ile Val Ile Met Ala Leu Arg Leu Ser Asp Asn Gly
100 105 110

Lys Tyr Thr Cys Ile Val Gln Lys Thr Glu Lys Arg Ser Tyr Lys Val 115 120 125

Lys His Met Thr Ser Val Met Leu Leu Val Arg Ala Asp Phe Pro Val 130 135 140

Pro Ser Ile Thr Asp Leu Gly Asn Pro Ser His Asp Ile Lys Arg Ile 145 150 155 160

Met Cys Ser Thr Ser Gly Gly Phe Pro Lys Pro His Leu Ser Trp Trp 165 170 175

Glu Asn Glu Glu Leu Asn Ala Ala Asn Thr Thr Val Ser Gln Asp 180 185 190

Pro Asp Thr Glu Leu Tyr Thr Ile Ser Ser Glu Leu Asp Phe Asn Ile 195 200 205

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Val Ser Gln Ile Phe Asn Trp Gln Lys Cys Lys 225 230 235

<210> 13

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<212> DNA

<213> Canis familiaris

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<213> Canis familiaris

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acagtgaaag aagtagcagt actgtcctgt gattacaaca tttccactac agaactgatg 180
aaagttcgaa tctattggca aaaggatgat gaagtggtgc tggctgtcac atctggacaa 240
acgaaagtgt ggtccaagta tgagaatcgc acctttgctg acttcaccaa taacctctcc 300
atcgtgatta tggctctgcg cctgtcagac aatggcaaat acacctgtat cgttcaaaaag 360
actgaaaaaa ggtcttacaa agtgaaacac atgacttcgg tgatgttatt ggtcagagct 420
gacttccctg tccctagtat aactgacctt ggaaatccat cccatgacat caaaaggata 480
atgtgttcaa cctctggagg ttttccaaaag cctcacctct cctggtgga aaatgaagaa 540
gaattgaatg ctgccaacac aacagtttcc caagacccgg acactgagtt gtacactatt 600
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<210> 15

<211> 705

<212> DNA

<213> Canis familiaris

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agtgtccggg tettgggaaa ctgttgtgtt ggcagcattc aattettett cattttccca 180

ccaggagagg tgaggetttg gaaaacctcc agaggttgaa cacattatcc ttttgatgtc 240
atgggatgga tttccaaggt cagttatact agggacaggg aagtcagete tgaccaataa 300
catcaccgaa gtcatgtgtt teactttgta agacctttt teagtettt gaacgataca 360
ggtgtatttg ccattgtetg acaggegag agccataate acgatggaga ggttattggt 420
gaagtcagca aaggtgegat teteatactt ggaccacact ttegtttgte cagatgtgac 480
agccagcacc acttcatcat cettttgcca atagattega acttcatca gttetgtagt 540
ggaaatgttg taatcacagg acagtactge tacttette actgtettgt teacetggat 600
gatgcctgaa cagaagtaaa agagactage tagcaccaag agctgagaga cettgagata 660



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tat ttc aac aag act gga gaa ctg cca tgc cat ttt aca aat tct caa Tyr Phe Asn Lys Thr Gly Glu Leu Pro Cys His Phe Thr Asn Ser Gln 35 40 45	144
aac ata agc ctg gat gag ttg gta gtg ttt tgg cag gac cag gat aag Asn Ile Ser Leu Asp Glu Leu Val Val Phe Trp Gln Asp Gln Asp Lys 50 55 60	192
ctg gtt ctg tac gag cta tac aga ggc aaa gag aac cct caa aat gtt Leu Val Leu Tyr Glu Leu Tyr Arg Gly Lys Glu Asn Pro Gln Asn Val 65 70 75	240
cat cgc aag tat aag ggc cgc aca agc ttt gac aaa gac aat tgg acc His Arg Lys Tyr Lys Gly Arg Thr Ser Phe Asp Lys Asp Asn Trp Thr 80 85 90	288
ctg aga ctc cat aat att cag atc aag gac aag ggc ttg tat caa tgt Leu Arg Leu His Asn Ile Gln Ile Lys Asp Lys Gly Leu Tyr Gln Cys 95 100 105 110	336
ttc gtt cat cat aaa ggg ccc aaa gga ctc gtt ccc atg cac cag atg Phe Val His His Lys Gly Pro Lys Gly Leu Val Pro Met His Gln Met 115 120 125	384
aat tot gad ota toa gtg ott got aad tto agt daa oot gaa ata atg Asn Ser Asp Leu Ser Val Leu Ala Asn Phe Ser Gln Pro Glu Ile Met	432

			130					135					140)		
			aat Asn					Ser								480
			caa Gln													528
			aat Asn													576
			gtc Val													624
			gaa Glu 210													672
			aag Lys													720
			aaa Lys													768
			aga Arg										-	_		816
			gac Asp							taat	taaa	iga g	taaa	igtcc	a	866
tcca	ittgt	tt	ıtatç	cctt	c cc	tttc	aaat	ttt	ggct	tgc	cttt	ttct	cg t	ccat	taata	926
ttat	tatt	gc d	cacta	ataa	ıt aa	ıgagç	jcttt	: cca	gggc	tcc	ctct	aaat	ga g	gagag	cctcc	986
ctat	aato	gcc a	agtto	tgct	c cc	taca	ccaç	g gag	ıcaga	ittt	taac	tgct	tc t	tttc	atctc	1046
agaç	gcaca	act t	gtgg	gcca	at go	ctcac	cctga	a ctç	gcto	ctg	gcto	agga	at a	aatgt	ttaag	1106
acta	acad	cct d	ectgt	ttca	ag at	tcaç	geett	ctt	ttct	taa	tttt	atac	at t	gtgt	tttat	1166

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<210> 17

<211> 280

<212> PRT

<213> Canis familiaris

<400> 17

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Asn Lys Thr Gly Glu Leu Pro Cys His Phe Thr Asn Ser Gln Asn Ile 35 40 45

Ser Leu Asp Glu Leu Val Val Phe Trp Gln Asp Gln Asp Lys Leu Val 50 60

Leu Tyr Glu Leu Tyr Arg Gly Lys Glu Asn Pro Gln Asn Val His Arg
65 70 75 80

Lys Tyr Lys Gly Arg Thr Ser Phe Asp Lys Asp Asn Trp Thr Leu Arg

85

90

95

Leu His Asn Ile Gln Ile Lys Asp Lys Gly Leu Tyr Gln Cys Phe Val

100 105 110

His His Lys Gly Pro Lys Gly Leu Val Pro Met His Gln Met Asn Ser 115 120 125

Asp Leu Ser Val Leu Ala Asn Phe Ser Gln Pro Glu Ile Met Val Thr 130 135 140

Ser Asn Arg Thr Glu Asn Ser Gly Ile Ile Asn Leu Thr Cys Ser Ser 145 150 155 160

Ile Gln Gly Tyr Pro Glu Pro Lys Glu Met Tyr Phe Leu Val Lys Thr 165 170 175

Glu Asn Ser Ser Thr Lys Tyr Asp Thr Val Met Lys Lys Ser Gln Asn 180 185 190

Asn Val Thr Glu Leu Tyr Asn Val Ser Ile Ser Leu Ser Phe Ser Val 195 200 205

Pro Glu Ala Ser Asn Val Ser Ile Phe Cys Val Leu Gln Leu Glu Ser 210 215 220

Met Lys Leu Pro Ser Leu Pro Tyr Asn Ile Glu Thr Asn Lys Val Glu 225 230 235 240

Arg Lys Glu Ser Glu Gln Thr Lys Glu Arg Val Arg Tyr His Glu Thr 245 250 255

Glu Arg Ser Asp Glu Ala Gln Cys Val Asn Ile Ser Lys Thr Ala Ser 260 265 270

Gly Asp Asn Ser Thr Thr Gln Phe 275 280

<210> 18

<211> 1795

<212> DNA

<213> Canis familiaris

<400> 18

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<210> 19

<211> 840

<212> DNA

<213> Canis familiaris

<400> 19

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gataagetgg ttetgtacga getatacaga ggeaaagaga acceteaaaa tgtteatege 240
aagtataagg geegeacaag etttgacaaa gacaattgga eeetgagaet eeataatatt 300
cagateaagg acaagggett gtateaatgt ttegtteate ataaagggee caaaggaete 360
gtteecatge accagatgaa ttetgaceta teagtgettg etaactteag teaacetgaa 420
ataatggtaa ettetaatag aacagaaaat tetggeatea taaatttgae etgeteatee 480
atacaaggtt acceagaace eaaggagatg tatttttgg taaaaacega gaatteaagt 540
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tetateaget tgteettee agteeetgaa geaageaatg tgageatet etgtgeeteg 660
caacttgagt eaatgaaget teeeteecta eettataata tagaaaceaa eaaagtggag 720
agaagaaagaaa gtgageagae caaggaaaga gtaeggtaee atgaaaegga aagatetgat 840
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<212> DNA

<213> Canis familiaris

<400> 20

<210> 21

<211> 18

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<220>

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<400> 21

gtcaragctg acttccct

18

<210> 22

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

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Stuff	House	,,,,,,,
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<223>	Description of Artificial Sequence: Synthetic Primer	
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	go att tgt gao ago act atg gga otg agt cao act oto ott gtg	226
Met G	ly Ile Cys Asp Ser Thr Met Gly Leu Ser His Thr Leu Leu Val	
7	5 10 15	

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Met	Ala	Leu	Leu 20	Leu	Ser	Gly	Val	Ser 25	Ser	Met	Lys	Ser	Gln 30	Ala	Tyr	
	aac Asn	_		,,	_	_		-								322
	agc Ser 50	_	-													370
_	ctg Leu															418
	aaa Lys															466
_	ctc Leu			_												514
	cat His															562
	gac Asp 130															610
	tct Ser															658
	ata Ile															706
	gag Glu			Thr												754
	aat Asn		Thr					Val					Pro			802

												ctg Leu		-		850
												gat Asp	_			898
												att Ile			_	946
	_	_		-	-		-		_			ttt Phe				994
			-	-	-	_						gaa Glu 285	-	-		1042
				-		-	-		_			gaa Glu	-	-		1090
		-			-		-	-	_	-	_	att Ile			_	1138
_		-			-		agt Ser					taat	taaa	iga		1184
ata	aagt	cca ·	tataa	actgi	tc ca	attgt	ttat	atç	jcctt	tcc	ctto	caagt	tt t	gggc	ttacc	1244
t _z tt	tttt	gtc	tatt	aata	tt at	tatt	acca	tta	ataa	atag	tgga	aggtt	cc a	aggac	tccat	1304
ctg	agaa	agc (cacc	ctgt	aa to	gccag	getet	gct	ccct	acc	tcaç	ggago	cag a	acctt	aactg	1364
ctt	cttt	tca	tttc	agag	ca aa	attt	gtgc	g cca	aagct	cac	ctga	actg	gat (cctg	gctcag	1424
gaa	taat	gtt	taag	acta	ac a	cctc	ctgtt	tca	acatt	cag	ccti	tcttt	itc 1	ttaat	tttat	1484
aaa	ttgc	gtc	ttat	gtag	aa c	tccc	aatta	a cto	ggaat	taat	ggc	tttt	atc '	tatgt	taattc	1544
taa	ggta	gtg	cctc	attc	ta t	cttg	tata	t tto	gtga	ctga	ata	acta	cct	cttca	agtctt	1604
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1

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<211> 332

<212> PRT

<213> Felis catus

<400> 26

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20 25 30

Phe Asn Lys Thr Gly Glu Leu Pro Cys His Phe Thr Asn Ser Gln Asn 35 40 45

Ile Ser Leu Asp Glu Leu Val Val Phe Trp Gln Asp Gln Asp Lys Leu 50 55 60

Val Leu Tyr Glu Ile Phe Arg Gly Lys Glu Asn Pro Gln Asn Val His . 65 70 75 80

Leu Lys Tyr Lys Gly Arg Thr Ser Phe Asp Lys Asp Asn Trp Thr Leu 85 90 95

Arg Leu His Asn Val Gln Ile Lys Asp Lys Gly Thr Tyr His Cys Phe 100 105 110

Ile His Tyr Lys Gly Pro Lys Gly Leu Val Pro Met His Gln Met Ser 115 120 125

Ser Asp Leu Ser Val Leu Ala Asn Phe Ser Gln Pro Glu Ile Thr Val 130 135 140

Thr Ser Asn Arg Thr Glu Asn Ser Gly Ile Ile Asn Leu Thr Cys Ser 145 150 155 160

Ser Ile Gln Gly Tyr Pro Glu Pro Lys Glu Met Tyr Phe Gln Leu Asn 165 170 175

Thr Glu Asn Ser Thr Thr Lys Tyr Asp Thr Val Met Lys Lys Ser Gln
180 185 190

Asn Asn Val Thr Glu Leu Tyr Asn Val Ser Ile Ser Leu Pro Phe Ser 195 200 205

Val Pro Glu Ala His Asn Val Ser Val Phe Cys Ala Leu Lys Leu Glu 210 215 220

Thr Leu Glu Met Leu Leu Ser Leu Pro Phe Asn Ile Asp Ala Gln Pro 225 230 235 240

Lys Asp Lys Asp Pro Glu Gln Gly His Phe Leu Trp Ile Ala Ala Val 245 250 255 Leu Val Met Phe Val Val Phe Cys Gly Met Val Ser Phe Lys Thr Leu 260 265 270

Arg Lys Arg Lys Lys Gln Pro Gly Pro Ser His Glu Cys Glu Thr 275 280 285

Ile Lys Arg Glu Arg Lys Glu Ser Lys Gln Thr Asn Glu Arg Val Pro 290 295 300

Tyr His Val Pro Glu Arg Ser Asp Glu Ala Gln Cys Ile Asn Ile Leu 305 310 315 320

Lys Thr Ala Ser Gly Asp Lys Ser Thr Thr His Phe 325 330

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<211> 2830

<212> DNA

<213> Felis catus

<400> 27

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<210> 28 <211> 996

<212> DNA

<213> Felis catus

<400> 28

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gtttctatca gcttgccttt ttcagtccct gaagcacaca atgtgagcgt cttttgtgcc 660 ctgaaactgg agacactgga gatgctgctc tccctacctt tcaatataga tgcacaacct 720 aaggataaag accctgaaca aggccacttc ctctggattg cggctgtact tgtaatgttt 780 gttgttttt gtgggatggt gtcctttaaa acactaagga aaaggaagaa gaagcagcct 840 ggcccctctc atgaatgtga aaccatcaaa agggagagaa aagaagacaa acagaccaac 900 gaaagagtac cataccacgt acctgagaga tctgatgaag cccagtgtat taacattttg 960 aagacagcct caggcgacaa aagtactaca catttt

<210> 29 <211> 996 <212> DNA <213> Felis catus

<400> 29

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atccaggett atgtttgag agtttgtaaa atggcatgge agtteteeag tettgttgaa 900 atatgettga etetteatgg aagaaacace agagageagg agggeeatea caaggagagt 960 gtgactcagt eccatagtge tgtcacaaat geecat 996

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Asn Val Thr Glu Leu Tyr Asn Val Ser Ile Ser Leu Pro Phe Ser Val
35 40 45

cct gaa gca cac aat gtg agc gtc ttt tgt gcc ctg aaa ctg gag aca 192
Pro Glu Ala His Asn Val Ser Val Phe Cys Ala Leu Lys Leu Glu Thr
50 55 60

ctg gag atg ctg ctc tcc cta cct ttc aat ata gat gca caa cct aag 240 Leu Glu Met Leu Leu Ser Leu Pro Phe Asn Ile Asp Ala Gln Pro Lys 65 70 75 80

gat aaa gac cct gaa caa ggc cac ttc ctc tgg att gcg gct gta ctt 288
Asp Lys Asp Pro Glu Gln Gly His Phe Leu Trp Ile Ala Ala Val Leu
85 90 95

gta atg ttt gtt gtt ttt tgt ggg atg gtg tcc ttt aaa aca cta agg 336 Val Met Phe Val Val Phe Cys Gly Met Val Ser Phe Lys Thr Leu Arg 100 105 110

aaa agg aag aag cag cct ggc ccc tct cat gaa tgt gaa acc atc 384

Lys Arg Lys Lys Gln Pro Gly Pro Ser His Glu Cys Glu Thr Ile 115 120 aaa agg gag aga aaa gag agc aaa cag acc aac gaa aga gta cca tac 432 Lys Arg Glu Arg Lys Glu Ser Lys Gln Thr Asn Glu Arg Val Pro Tyr 130 135 cac gta cct gag aga tct gat gaa gcc cag tgt att aac att ttg aag 480 His Val Pro Glu Arg Ser Asp Glu Ala Gln Cys Ile Asn Ile Leu Lys 145 150 155 aca gcc tca ggc gac aaa agt act aca ca 509 Thr Ala Ser Gly Asp Lys Ser Thr Thr 165 <210> 31 <211> 169 <212> PRT <213> Felis catus <400> 31 Ile Gln Gly Tyr Pro Glu Pro Lys Glu Met Tyr Phe Gln Leu Asn Thr Glu Asn Ser Thr Thr Lys Tyr Asp Thr Val Met Lys Lys Ser Gln Asn 25 Asn Val Thr Glu Leu Tyr Asn Val Ser Ile Ser Leu Pro Phe Ser Val 35 40 45 Pro Glu Ala His Asn Val Ser Val Phe Cys Ala Leu Lys Leu Glu Thr 55 Leu Glu Met Leu Leu Ser Leu Pro Phe Asn Ile Asp Ala Gln Pro Lys 70 Asp Lys Asp Pro Glu Gln Gly His Phe Leu Trp Ile Ala Ala Val Leu 85 90 Val Met Phe Val Val Phe Cys Gly Met Val Ser Phe Lys Thr Leu Arg 100 105 Lys Arg Lys Lys Gln Pro Gly Pro Ser His Glu Cys Glu Thr Ile 115 120 Lys Arg Glu Arg Lys Glu Ser Lys Gln Thr Asn Glu Arg Val Pro Tyr

140

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<210> 32

<211> 509

<212> DNA

<213> Felis catus

<400> 32

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cttttgatgg tttcacattc atgagagggg ccaggctgct tcttcttcct tttccttagt 180

gttttaaagg acaccatccc acaaaaaaca acaaacatta caagtacagc cgcaatccag 240

aggaagtggc cttgttcagg gtctttatcc ttaggttgtg catctatatt gaaaggtagg 300

gagagcagca tetecagtgt etecagttte agggeacaaa agaegeteae attgtgtget 360

tcagggactg aaaaaggcaa gctgatagaa acgttgtaca gttctgtcac attattttga 420

gatttcttca tgacagtatc atacttagta gttgaattct cagtgtttag ctgaaaatac 480

atctccttag gttctgggta accttgtat 509

<210> 33

<211> 359

<212> DNA

<213> Felis catus

<220>

<221> CDS

<222> (1)..(357)

<400> 33

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Ile Gln Gly Tyr Pro Glu Pro Lys Glu Met Tyr Phe Gln Leu Asn Thr

1 5 10 15

gag aat toa act act aag tat gat act gto atg aag aaa tot caa aat 96

Glu	Asn	Ser	Thr 20	Thr	Lys	Tyr	Asp	Thr 25	Val	Met	Lys	Lys	Ser 30	Gln	Asn	
		aca Thr 35	_													144
		gca Ala														192
_	, ,	atg Met	_								-					240
		aaa Lys														288
		aga Arg														336
		gac Asp 115		-			ca									359
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	0> 3	4 G1 v		Pro	Glu	Pro	I.ve	Glu	Met	Tvr	Phe	Gln	Leu	Asp	Thr	

Ile Gln Gly Tyr Pro Glu Pro Lys Glu Met Tyr Phe Gln Leu Asn Thr

Glu Asn Ser Thr Thr Lys Tyr Asp Thr Val Met Lys Lys Ser Gln Asn 20. 25 30

Asn Val Thr Glu Leu Tyr Asn Val Ser Ile Ser Leu Pro Phe Ser Val 35 40 45

Pro Glu Ala His Asn Val Ser Val Phe Cys Ala Leu Lys Leu Glu Thr 50 55 60

Leu Glu Met Leu Leu Ser Leu Pro Phe Asn Ile Glu Thr Ile Lys Arg 65 70 75 80

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Glu Arg Lys Glu Ser Lys Gln Thr Asn Glu Arg Val Pro Tyr His Val
85 90 95
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Pro Glu Arg Ser Asp Glu Ala Gln Cys Ile Asn Ile Leu Lys Thr Ala 100 105 110

Ser Gly Asp Lys Ser Thr Thr 115

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<400> 35

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<212> DNA

<213> Felis catus

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<221> CDS

<222> (1)..(522)

<400> 36

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ccc aag ctc ttt ccg ctc ttg atg cta gct agt ctt ttt tac ttc tgt 96
Pro Lys Leu Phe Pro Leu Leu Met Leu Ala Ser Leu Phe Tyr Phe Cys
20 25 30

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		atc Ile 35														144
		gat Asp												_		192
		caa Gln														240
		gtg Val											-	-		288
		cac His											-			336
		act Thr 115														384
		ctg Leu													-	432
		ccc Pro		-					_		-		_	_		480
_		gag Glu	-	_		_	_		-			-	tga			522
gcca	accc	agg (catc	ccaat	tg at	tactt	tcta	a aat	aaad	ctct	taaa	aaaa	aa a	aaaa	aaaaa	582
aaa	aaaa	aaa .	aa													594

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<211> 173

<212> PRT .

<213> Felis catus

<400> 37

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Ser Gly Ile Ile Gln Val Asn Lys Thr Val Glu Glu Val Ala Val Leu 35 40 45

Ser Cys Asp Tyr Asn Ile Ser Thr Lys Glu Leu Thr Glu Ile Arg Ile 50 55 60

Tyr Trp Gln Lys Asp Asp Glu Met Val Leu Ala Val Met Ser Gly Lys 65 70 75 80

Val Gln Val Trp Pro Lys Tyr Lys Asn Arg Thr Phe Thr Asp Val Thr
85 90 95

Asp Asn His Ser Ile Val Ile Met Ala Leu Arg Leu Ser Asp Asn Gly
100 105 110

Lys Tyr Thr Cys Ile Ile Gln Lys Ile Glu Lys Gly Ser Tyr Lys Val

Lys His Leu Thr Ser Val Met Leu Leu Val Arg Gly Val Thr Pro Ser 130 135 140

Thr Glu Pro Asn Ala His Ala Glu Leu Glu Ile Met Thr Leu Arg Ser 145 150 155 160

Arg Pro Glu Leu Arg Ser Arg Val Gly Arg Leu Ile Asp 165 170

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<210> 40

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<212> DNA

<213> Felis catus

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<400> 40

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Met Thr Glu Val Cys Ala Ala Thr Tyr Thr Val Glu Asp Glu Leu Ala

atg act gaa gtc tgt gcc gcg aca tac aca gtg gag gat gag ttg gcc 347

				85					90					95		
														aaa Lys		395
														tac Tyr		443
-	_													atg Met		491
			_											gat Asp		539
,							-	-	-	_				ttt Phe 175		587
														aag Lys		635
														act Thr		683
	-	_	gaa Glu	_										aat Asn	tga	731
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ttt	gtgc	tat	ccag	ctat	gt g	tact	tgtt	t gt	atat	tttg	ggg	gggg.	ttt (catc	tctctt	851
taa	tata	aag	ctgg	atgc	ag a	accc	aaat	g aa	gtgt	acta	caa	attc	aaa	gcaa	aggtgc	911
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WO 99/47558 PCT/US99/06187

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<211> 223

<212> PRT

<213> Canis familiaris

<400> 42

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Ser Arg Thr Trp Pro Cys Thr Ala Leu Phe Ser Leu Leu Phe Ile Pro
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Val Phe Ser Lys Gly Met His Val Ala Gln Pro Ala Val Leu Ala 35 40 45

Ser Ser Arg Gly Val Ala Ser Phe Val Cys Glu Tyr Gly Ser Ser Gly 50 55 60

Asn Ala Ala Glu Val Arg Val Thr Val Leu Arg Gln Ala Gly Ser Gln 65 70 75 80

Met Thr Glu Val Cys Ala Ala Thr Tyr Thr Val Glu Asp Glu Leu Ala 85 90 95 Phe Leu Asp Asp Ser Thr Cys Thr Gly Thr Ser Ser Gly Asn Lys Val
100 105 110

Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile 115 120 125

Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Val Gly Met Gly
130 135 140

Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser 145 150 155 160

Asp Phe Leu Leu Trp Ile Leu Ala Ala Val Ser Ser Gly Leu Phe Phe 165 170 175

Tyr Ser Phe Leu Ile Thr Ala Val Ser Leu Ser Lys Met Leu Lys Lys 180 185 190

Arg Ser Pro Leu Thr Thr Gly Val Tyr Val Lys Met Pro Pro Thr Glu 195 200 205

Pro Glu Cys Glu Lys Gln Phe Gln Pro Tyr Phe Ile Pro Ile Asn 210 215 220

<210> 43

<211> 1856

<212> DNA

<213> Canis familiaris

<400> 43

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tocataaaac ttcccctgag cccctggtgg gaagacactg ccatatagtg tttatattga 540 aaccatcaac aaatacacaa aagcacatgt ggcccccatg cataatacta tcagataaaa 600 aaatatatat tggtacaata caacctttgg aatcactggc taaaatatag ccatgtgaat 660 atttttaaag tottcacgtg attttacatt tatgaaaaat aacatagcac aaaaatttaa 720 cttgaaaacg tcacttcagc tataaacttc tcacatgtaa atacaaagtg tgtacaatat 780 catectetee etgaetetet eteetttget ttetttggae egeaceaete eetaacetat 840 atcctagage geatgtecta atgctgeate eccatattge teccaagtga tacttttaeg 900 aaaattggat ctgatgtgac agaaacatcc tggctctgtt ttcttgcacc tttgctttga 960 atttgtagta cacttcattt gggttctgca tccagcttta tattaaagag aqatgaaacc 1020 cccccaaaa tatacaaaca agtacacata gctggatagc acaaagttag aattgcctca 1080 gctcctggaa attggaaaat attctttctt cttcataatg atctctcaat tgatgggaat 1140 aaaataaggc tgaaattgct tttcacattc tggctcagtt gggggcattt tcacatagac 1200 ccctgtggta agagggcttc ttttctttag cattttgctc aaagaaacag ctgtgataag 1260 aaagctataa aaaaacaagc ccgaactgac tgctgcaagg atccagagga ggaagtcaga 1320 atctggqcaa qqttcaggat cgatgacata aatctgggtt ccatttccca tgcctacata 1380 gtagggtggt gggtacatga gctccacctt gcagatgtag agccccgtgt ccatggccct 1440 caaccettqq atqqtqaqqt tcactttqtt tccactggag gtgccggtgc aggtagaatc 1500 atccaggaag gccaactcat cctccactgt gtatgtcgcg gcacagactt cagtcatctg 1560 getgecagee tgeegeagea etgteaceeg gaeetegget gegttgeetg aagaeeeata 1620 ttcacacacg aagctagcaa caccccggct gctggccaga accactgcag gctgagccac 1680 ggtcctagaa gccaggtccg gctgagcccc atgcctccgg aatccaaagc cagccatggc 1800 tttatggage agtgttcagg tettcaggaa gcagagtgaa acetttcagg atectg 1856 <211> 669

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<213> Canis familiaris

<400> 44

<210> 45

<211> 669

<212> DNA

<213> Canis familiaris

<400> 45

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agetgtgata agaaagetat aaaaaacaa geeegaactg actgetgeaa ggateeagag 180

gaggaagtea gaatetggge aaggtteagg ategatgaca taaatetggg tteeatttee 240

catgeetaca tagtagggtg gtgggtacat gageteeace ttgeagatgt agageeeggt 300

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Met Ala Cys Phe Gly Phe Arg Arg His Gly Ala Gln Leu Asp

1 5 10

ctg gct tct agg acc tgg ccc tgc act gct ctg ttt tct ctt ctc ttt 158

Leu Ala Ser Arg Thr Trp Pro Cys Thr Ala Leu Phe Ser Leu Leu Phe

15 20 25 30

atc ccc gtc ttc tcc aaa ggg atg cat gtg gcc cag cct gca gtg gtg 206

Ile Pro Val Phe Ser Lys Gly Met His Val Ala Gln Pro Ala Val

35 40 45

ctg gcc agc cga ggt gtc gcc agc ttc gtg tgt gaa tat ggg tct 254

Leu Ala Ser Ser Arg Gly Val Ala Ser Phe Val Cys Glu Tyr Gly Ser

50 55 60

tca ggc aat gcc gcc gaa gtc cga gtg act gtg ctg agg cag act ggc 302 Ser Gly Asn Ala Ala Glu Val Arg Val Thr Val Leu Arg Gln Thr Gly
65 70 75

agc cag atg act gaa gtc tgt gct gcg aca tac aca gtg gag aat gag 350 Ser Gln Met Thr Glu Val Cys Ala Ala Thr Tyr Thr Val Glu Asn Glu 80 85 90

					gat Asp 100											398
					atc Ile											446
					gag Glu											494
					cag Gln											542
					ctc Leu											590
					ctt Leu 180											638
					ctt Leu											686
					gaa Glu											734
aat Asn		cac	accg	tta	tgaa	gaag	ga a	gaac	actg	t cca	aatt [.]	tcta	aga	gctga	agg	790
caa	ttct	aac	tttt	tgct	at c	cagc	tatg	t tg	ctta	tttg	tgt	attt	tgg	gggg	ggattc	850
ato	tctc	ttt	aata	taaa	gc t	ggat	gcaa	a at	ccag	atga	agt	gtac	tac	aatt	tgaagc	910
aaa	aggto	gcag	gaaa	acag	ag c	cagg	atgt	t tc	tgtc	acat	cag	atcc	aat	ttta	gtaaaa	970
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															ttgtac	
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<211> 223

<212> PRT

<213> Felis catus

<400> 47

Met Ala Cys Phe Gly Phe Arg Arg His Gly Ala Gln Leu Asp Leu Ala 1 5 10 15

Ser Arg Thr Trp Pro Cys Thr Ala Leu Phe Ser Leu Leu Phe Ile Pro 20 25 30

Val Phe Ser Lys Gly Met His Val Ala Gln Pro Ala Val Val Leu Ala 35 40 45

Ser Ser Arg Gly Val Ala Ser Phe Val Cys Glu Tyr Gly Ser Ser Gly 50 55 60

Asn Ala Ala Glu Val Arg Val Thr Val Leu Arg Gln Thr Gly Ser Gln 65 70 75 80

Met Thr Glu Val Cys Ala Ala Thr Tyr Thr Val Glu Asn Glu Leu Ala 85 90 95

Phe Leu Asp Asp Ser Thr Cys Thr Gly Ile Ser Ser Gly Asn Lys Val 100 105 110

Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile 115 120 125

Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Ala Gly Met Gly
130 135 140

Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser 145 150 155 160

Asp Phe Leu Leu Trp Ile Leu Ala Ala Val Ser Ser Gly Leu Phe Phe 165 170 175

Tyr Ser Phe Leu Ile Thr Ala Val Ser Leu Ser Lys Met Leu Lys Lys 180 185 190

Arg Ser Pro Leu Thr Thr Gly Val Tyr Val Lys Met Pro Pro Thr Glu
195 200 205

Pro Glu Cys Glu Lys Gln Phe Gln Pro Tyr Phe Ile Pro Ile Asn 210 215 220

<210> 48

<211> 1883

<212> DNA

<213> Felis catus

<400> 48

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agagcttcct tgaagttcgt acctacaaga cccctggagt gagccatttt cttgaggttg 300
gtgttctatt gaattacatc agatacacca gtctggactc ccttgcaaac ctttgaaagg 360
agctaacata aaagcccaaa tcacatgtca acaccaattc agctcaacgt gtctataaga 420

4 to 12

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cctttcagga tcctgaagct ttg

1883

<210> 49

<211> 669

<212> DNA

<213> Felis catus

<400> 49

<210> 50

<211> 669

<212> DNA

<213> Felis catus

<400> 50

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<220>

<223> Description of Artificial Sequence: Synthetic Primer

<400> 51 atacaaggtt acccagaacc

20

<210> 52 <211> 20 <212> DNA <213> Artificial Sequence

<223> Description of Artificial Sequence: Synthetic Primer

<400> 52 tgtgtagtac ttttgtcgcc

20

<210> 53 <211> 34 <212> DNA <213> Artificial Sequence

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	<210>	5.4		
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#(S	ccctc	gaget atgtagacag gtgagate		28
#1: #:4				20
	<210>	55		
rii	<211>			
Harry Marie	<212>			
F ==		Artificial Sequence		
Aller Mark aller H.				
Het.	<220>		\	
		Description of Artificial Sequence:	Synthetic	
		Primer	.,	
	<400>	55		
	gtaata	acgac tcactatagg gc		22
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	<211>	20		
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en.	<210> 58		
5% 417	<211> 31		
ř1	<212> DNA		
ows (west soul-state) and that they that	<213> Artificial Sequence		
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T I	<223> Description of Artificial Sequence:	Synthetic	
şİ.	Primer		
#3 #3	<400> 58		
The state of	gcggatccac catgggcatt tgtgacagca c		31
ell ell			
FA FA	•		
si.	<210> 59		
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i Pile	<400>	61		
gering (1976), glave H. H. glave Hanne Han	gcatt	ttcac atagacccct g		21
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[]	<212>	DNA		
ė nįs	<213>	Artificial Sequence		
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: # 2 ·	<400>	62		
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	ccgaa	tices agreagate tyggeaaggt to		32
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28

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<210> 65 <211> 35

<212> DNA

<213> Artificial Sequence

<220>

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